

In the Claims:

Please cancel claim 1 without prejudice or disclaimer.

Please add the following new claims:

- A7
- 28. A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:
- (A) receiving a protein backbone structure;
  - (B) establishing a group of potential rotamers for each of said variable residue positions wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and
  - (C) analyzing the interaction of each of said rotamers with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences, wherein said analyzing step includes a forcefield calculation.
29. A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:
- (A) receiving a protein backbone structure;
  - (B) establishing a group of potential rotamers for each of said variable residue positions wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and
  - (C) analyzing the interaction of either or both of :
    - i) each of said rotamers with all or part of the remainder of said protein backbone structure; and
    - ii) each of said rotamers with all or part of the remainder of the rotamers for each amino acid at each position of said protein;to generate a set of optimized protein sequences, wherein said analyzing step includes a forcefield calculation.
30. A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

- A2  
cont
- (A) receiving a protein backbone structure;
  - (B) establishing a group of potential rotamers for each of said variable residue positions wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and
  - (C) analyzing the interaction of either or both of:
    - i) each of said rotamers with all or part of the remainder of said protein backbone structure; and
    - ii) each of said rotamers with all or part of the remainder of the rotamers for each amino acid at each position of said protein;
- to generate a set of optimized protein sequences; and
- (D) identifying residues in at least one of said optimized protein sequences that differ from the starting backbone.

31. A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

- (A) receiving a protein backbone structure;
  - (B) establishing a group of potential rotamers for each of said variable residue positions wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and
  - (C) analyzing the interaction of either or both of:
    - i) each of said rotamers with all or part of the remainder of said protein backbone structure; and
    - ii) each of said rotamers with all or part of the remainder of the rotamers for each amino acid at each position of said protein;
- to generate a set of optimized protein sequences, wherein said analyzing step includes a forcefield calculation; and
- (D) identifying residues in at least one of said optimized protein sequences that differ from the starting backbone.